

Claims:

1. A method of screening for an agent that modulates the differentiation into osteoblasts, comprising: (a) preparing a first gene or gene family expression profile of a cell population comprising MC3T3-E1 or MC3T3-1b cells and/or assaying an activity of a protein encoded by at least one gene or a member of a gene family of Table 1 of a cell population comprising MC3T3-E1 or MC3T3-1b cells; (b) exposing the cell population to the agent; (c) preparing second gene or gene family expression profile of the agent exposed cell population and/or assaying an activity of a protein encoded by at least one gene or a member of a gene family of Table 1 of the exposed cell population; and (d) comparing the first and second expression profiles or first and second activities to an expression profile and/or an activity of an osteoblastic differentiated MC3T3-E1 or MC3T3-1b cell population.
2. The method of claim 1, wherein the gene expression profiles comprise the expression levels for a set of genes that are differentially regulated in MC3T3-E1 or MC3T3-1b cells compared to an osteoblastic differentiated MC3T3-E1 or MC3T3-1b cell population.
3. The method of claim 1, wherein the agent modulates the level of expression or activity for at least one gene in the MC3T3-E1 or MC3T3-1b cell population to the expression level found in an osteoblastic differentiated MC3T3-E1 or MC3T3-1b cell population.
4. The method of claim 1, wherein the gene expression profiles or activity level comprise the expression or activity levels in a cell of at least two genes or members of a gene family in Table 1.
5. The method of claim 1, wherein the gene is Hey1.
6. A method of diagnosing a condition characterized by abnormal deposition of bone tissue, comprising detecting in a tissue sample the level of expression of and/or activity of a protein encoded by at least one gene or member of a gene family of

Table 1, wherein differential expression or activity of the gene or member of a gene family is indicative of abnormal bone tissue deposition.

7. A method of monitoring the treatment of a patient with a condition characterized by abnormal bone tissue deposition, comprising: (a) administering a pharmaceutical composition to the patient; (b) preparing a gene expression profile from a cell or tissue sample from the patient and/or assaying an activity of a protein encoded by at least one gene or a member of a gene family of Table 1; and (c) comparing the patient expression profile or activity to an expression profile or activity from a MC3T3-E1 or MC3T3-1b cell population or an osteoblastic differentiated MC3T3-E1 or MC3T3-1b cell population.
8. A method of diagnosing a condition characterized by an abnormal rate of formation of osteoblasts, comprising detecting in a tissue sample a level of expression of and/or activity of a protein encoded by at least one gene or member of a gene family from Table 1, wherein differential expression and/or activity of the gene or member of a gene family is indicative of an abnormal rate of formation of osteoblasts.
9. A method of monitoring the treatment of a patient with a condition characterized by abnormal rate of formation of osteoblasts, comprising: (a) administering a pharmaceutical composition to the patient; (b) preparing a gene expression profile and/or assaying an activity of at least one gene or member of a gene family from Table 1 in a cell or tissue sample from the patient; and (c) comparing the patient gene expression profile and/or activity to a gene expression profile or activity from a MC3T3-E1 or MC3T3-1b cell population or an osteoblastic differentiated MC3T3-E1 or MC3T3-1b cell population.
10. A method of diagnosing osteoporosis in a patient, comprising detecting the level of expression and/or activity in a tissue sample of at least one gene or member of a gene family from Table 1; wherein differential expression or activity is indicative of osteoporosis.
11. A method of monitoring the treatment of a patient with osteoporosis, comprising: (a) administering a pharmaceutical composition to the patient; (b) preparing a gene

expression profile and/or assaying an activity of at least one gene or member of a gene family of Table 1 in a cell or tissue sample from the patient; and (c) comparing the patient gene expression profile and/or activity to a gene expression profile or activity in a MC3T3-E1 or MC3T3-1b cell population and/or an osteoblastic differentiated MC3T3-E1 or MC3T3-1b cell population.

12. A method of screening for an agent capable of ameliorating the effects of osteoporosis, comprising: (a) exposing a cell to the agent; and (b) detecting the expression and/or activity level of one or more genes or members of a gene family of Table 1.
13. A method of monitoring the progression of bone tissue deposition in a patient, comprising detecting the level of expression and/or activity in a tissue sample of at least one gene or member of a gene family from Table 1; wherein differential expression and/or activity is indicative of bone tissue deposition.
14. A method of screening for an agent capable of modulating the deposition of bone tissue, comprising: (a) exposing a cell to the agent; and (b) detecting the expression and/or activity level of at least one gene or member of a gene family of Table 1.
15. The method of any one of claims 1-14, wherein expression and/or activity levels of at least 2 genes are detected.
16. The method of any one of claims 1-14, wherein expression and/or activity levels of at least 3 genes are detected.
17. The method of any one of claims 1-15, wherein expression and/or activity levels of at least 4, 5, 6, 7, 8, 9, 10 or 11 genes are detected.
18. The method of any one of claims 1-14, wherein expression and/or activity levels of all the genes in Table 1 are detected.
19. The method of any one of claims 1-14, wherein expression and/or activity levels of all the genes in Table 2 are detected.

20. The method of any one of claims 1-14, wherein expression and/or activity levels of all the genes in Table 3 are detected.
21. A composition comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.
22. The composition according to claim 21, wherein the composition comprises at least 3 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.
23. The composition according to claim 21, wherein the composition comprises at least 5 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.
24. The composition according to claim 21, wherein the composition comprises at least 7 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.
25. The composition according to claim 21, wherein the composition comprises at least 10 oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.
26. The composition according to any one of claims 21-25, wherein the oligonucleotides are attached to a solid support.
27. The composition according to claim 25, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material and a silicon support.
28. A solid support to which is attached at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene or member of a gene family of Table 1.

29. The solid support according to claim 28, wherein at least one oligonucleotide is attached covalently.
30. The solid support according to claim 28, wherein at least one oligonucleotide is attached non-covalently.
31. The solid support of claim 28, wherein the solid support is an array comprising at least 10 different oligonucleotides in discrete locations per square centimeter.
32. The solid support of claim 28, wherein the array comprises at least 100 different oligonucleotides in discrete locations per square centimeter.
33. The solid support of claim 28, wherein the array comprises at least 1000 different oligonucleotides in discrete locations per square centimeter.
34. The solid support of claim 28, wherein the array comprises at least 10000 different oligonucleotides in discrete locations per square centimeter.
35. A computer system comprising: (a) a database containing information identifying the expression and /or activity level in osteoblasts of a set of genes comprising one or more genes or members of a gene family in Table 1; and (b) a user interface to view the information.
36. The computer system of claim 35, wherein the database further comprises sequence information for the genes or gene families.
37. The computer system of claim 35, wherein the database further comprises information identifying the expression and/or activity level in MC3T3-E1 and/or MC3T3-1b cells of at least one gene or member of a gene family of Table 1.

38. The computer system of claim 35, wherein the database further comprises information identifying the expression level a set of genes indicative of a condition characterized by abnormal bone tissue deposition.
39. The computer system of any of claims 35-38, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.
40. The computer system of claim 39, wherein the external database is GenBank.
41. The method of using a computer system of any one of claims 35-40 to present information identifying the expression level in a tissue or cell of a set of genes comprising at least two of the genes or members of gene families in Table 1, comprising: (a) comparing the expression level of at least one gene or member of a gene family in Table 1 in the tissue or cell to the level of expression of the gene in the database.
42. The method of claim 41, wherein the expression levels of at least two genes are compared.
43. The method of claim 41, wherein the expression levels of at least five genes are compared.
44. The method of claim 41, wherein the expression levels of at least ten genes are compared.
45. The method of claim 41, further comprising the step of displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level in osteoblastic differentiated MC3T3-E1 cells and/or MC3T3-1b cells.